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(1) GENERAL INFORMATION:

- (i) APPLICANT: Simons, Michael
Volk, Rudiger
Horowitz, Arie
- (ii) TITLE OF INVENTION: Stimulation of angiogenesis
via enhanced endothelial expression of syndecan-4
core proteins
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David Prashker, Esq.
 - (B) STREET: P.O. Box 5387
 - (C) CITY: Magnolia
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 01930
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
 - (B) COMPUTER: Dell PC
 - (C) OPERATING SYSTEM: MS DOS
 - (D) SOFTWARE: Microsoft Word version 97
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/145,916
 - (B) FILING DATE: September 2, 1998
 - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: David Prashker, Esq.
 - (B) REGISTRATION NUMBER: 29,693
 - (C) REFERENCE/DOCKET NUMBER: BIS-039
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 762 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGGCGCTCTG GCTTTGGCTC TGC GCGCTGG CGCTGCGCCT GCAGCCTGCC 60
CTCCCGCAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120
TCAGACAACT TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
ACCAGCAGGG ATACCGAGGC CACCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
GAGGGAGAGC CCGTGGCCCA CGTGGAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCTCA 420
ACAGCAGCCA GAGCCACGAC GGCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG 480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAGACT TCACCTTTGA AACATCTGGG 660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
GGAGCCACAG GTGCTTCTCA GGCCTTTTG GACAGGAAGG AA 762

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1020 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
GAGGCGCGGC GCGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
GCTGCTCTCC AGATACCCCC GGAGCTCCAG CCGCGCGGAT CGCGCGCTCC CGCCGCTCTG 180
CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCTT AAAACCAGAA 240
ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
AGCTTCAGAG AGCAGCCTTC CCGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
AGTGAGAGGG CGCCGCGTTC CCGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
AGGAAGCGAG CGCCCCCGAG CCCCAGAGCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
GGTACTCTGC TCCGGATTCT TGTGCGCGGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGGAATAT GCGGCGCGCG 600
TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCCTGTCGG CGGAGTCGAG AGCAGAGCTG 660
ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
AGTCCAGAGC TGACAACAAC TCGACCACTT CCAAAGATAC TGTTGACTAG TGCTGCTCCA 840
AAAGTGGAAA CCACGACGCT GAATATACAG AACAAAGATAC CTGCTCAGAC AAAGTCACCT 900
GAAGAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTTAA ACGGACAGAA 1020

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

31
Cont

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Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Glu Lys Glu Glu
1          5          10          15
Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
20          25          30
Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
35          40          45
Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
50          55          60
Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
65          70          75          80
Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
85          90          95
Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
100         105         110
Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
115         120         125
Gly Ala Ala Ala Gly Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
130         135         140
Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
145         150         155         160
Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
165         170         175
Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Ala Gly Ser Ser Arg
180         185         190
Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
195         200         205
Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
210         215         220

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Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
 225 230 235 240
 Pro Ile Asp Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
 245 250 255
 Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Thr Arg Pro Leu Pro Lys
 260 265 270
 Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Thr Leu Asn
 275 280 285
 Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
 290 295 300
 Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
 305 310 315 320
 Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
 325 330 335
 Lys Arg Thr Glu
 340

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCGCGCGGAG CTGCGGCGCC 60
 TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
 AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
 ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
 TGGAGACAGC GGTGAGCCTC ACCACGGACA CGTCCGTCCC ACTGCCACC ACCGTGGCCG 300
 TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCTT TGAGCTGTTC CCCACAGAGG 360
 ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAG 420
 TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
 CCTCCACCAC CACCACCACG GCTGCTACCA CCACCACAAC CACCACCACC ATCAGCACCA 540
 CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCTT GCGCGGCTTT GTCACCAAGG 600
 CAGCCACCAC CCGGGCCACC ACCCTGGAGA CGCCACCAC CTCCATCCCT GAAACCAGTG 660
 TCCTGACAGA GGTGACCACA TCACGGCTTG TCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
 TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAAGCACT GCCTTGCCTT 780
 CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
 CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCAGCGGG GACTTCGAGA 900
 TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGGCAA TGAGGTGGTG GCAGTGGTGA 960
 CACCACCAGC AGCACCAGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
 TAGAGTCGGG CAGCTCGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
 GCGCCAGGCG AGTCGATTCG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
 AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCTTGA GCAGGACTCT 180
 GACTTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCCAG GACCTTCCCT 240
 GAGGTGATTT CACCCTTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300

ATCCGTGTCC CCTCAGAGCC CAAGGAACTG GAAGAGAATG AGGTCATTCC CAAAAGGGTC 360
 CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
 GGCAGCAACA TTTTGTAAAG AACTGAG 447

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
 GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
 GCTAAGGGCT TTAGCCTGAG CGACGTGCCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
 ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
 AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
 GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
 AACTGCAAGG ATGCTTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
 TTCCGGGACC TGTATGCTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
 GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
 CAGCTTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGGCA AGCAGGCAGA GGCACTGCGG 600
 CCGTTTGGGG ATGCCCTCTG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
 CGATCCTTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCAGGTT 720
 CCTCTGGCCC CAGAATGTTT TCGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCCGG 780
 GGAGTCCCTG GTGCCCGGCC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
 GCCAACCAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
 ACTGACAAGT TCTGGGGCCC GTCGGGTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
 CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAGGACA CACTCACAGC TAAGGTCATC 1020
 CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
 CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGTCTCT 1140
 GAGGCCAAGG CCCAGCTCCG AGACATTGAG GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
 TGTAAGTGAGA AGATGGCCAT GAGTCCTGCC AGCGATGACC GCTGCTGGAA TGGGATTTCC 1260
 AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCCT 1320
 GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
 AAGATCATGA CCAACCGTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
 GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
 CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCTT TGACCCATGC CCTCCCCGGC 1560
 TTGTCAGAAC AGGAGGGACA GAAGACCTCG 1590

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
 1 5 10 15
 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
 20 25 30
 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 35 40 45
 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 50 55 60
 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His

65					70					75					80
Ser	Arg	Met	Glu	Leu	Glu	Thr	Ala	Leu	His	Asp	Ser	Ser	Arg	Ala	Leu
				85					90					95	
Gln	Ala	Thr	Leu	Ala	Thr	Gln	Leu	His	Gly	Ile	Asp	Asp	His	Phe	Gln
			100					105					110		
Arg	Leu	Leu	Asn	Asp	Ser	Glu	Arg	Thr	Leu	Gln	Asp	Ala	Phe	Pro	Gly
		115					120					125			
Ala	Phe	Gly	Asp	Leu	Tyr	Thr	Gln	Asn	Thr	Arg	Ala	Phe	Arg	Asp	Leu
	130					135					140				
Tyr	Ala	Glu	Leu	Arg	Leu	Tyr	Tyr	Arg	Gly	Ala	Asn	Leu	His	Leu	Glu
145					150				155					160	
Glu	Thr	Leu	Ala	Glu	Phe	Trp	Ala	Arg	Leu	Leu	Glu	Arg	Leu	Phe	Lys
				165					170					175	
Gln	Leu	His	Pro	Gln	Leu	Leu	Leu	Pro	Asp	Asp	Tyr	Leu	Asp	Cys	Leu
			180					185					190		
Gly	Lys	Gln	Ala	Glu	Ala	Leu	Arg	Pro	Phe	Gly	Asp	Ala	Pro	Arg	Glu
		195					200					205			
Leu	Arg	Leu	Arg	Ala	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Ser	Phe	Val
	210					215					220				
Gln	Gly	Leu	Gly	Val	Ala	Ser	Asp	Val	Val	Arg	Lys	Val	Ala	Gln	Val
225				230						235				240	
Pro	Leu	Ala	Pro	Glu	Cys	Ser	Arg	Ala	Val	Met	Lys	Leu	Val	Tyr	Cys
			245					250						255	
Ala	His	Cys	Arg	Gly	Val	Pro	Gly	Ala	Arg	Pro	Cys	Pro	Asp	Tyr	Cys
			260				265						270		
Arg	Asn	Val	Leu	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	Ala
	275						280					285			
Glu	Trp	Arg	Asn	Leu	Leu	Asp	Ser	Met	Val	Leu	Ile	Thr	Asp	Lys	Phe
	290					295				300					
Trp	Gly	Pro	Ser	Gly	Ala	Glu	Asn	Val	Ile	Gly	Ser	Val	His	Met	Trp
305				310						315				320	
Leu	Ala	Glu	Ala	Ile	Asn	Ala	Leu	Gln	Asp	Asn	Lys	Asp	Thr	Leu	Thr
				325					330					335	
Ala	Lys	Val	Ile	Gln	Gly	Cys	Gly	Asn	Pro	Lys	Val	Asn	Pro	His	Gly
			340					345					350		
Ser	Gly	Pro	Glu	Glu	Lys	Arg	Arg	Arg	Gly	Lys	Leu	Ala	Leu	Gln	Glu
	355						360					365			
Lys	Ser	Ser	Thr	Gly	Thr	Leu	Glu	Lys	Leu	Val	Ser	Glu	Ala	Lys	Ala
	370					375					380				
Gln	Leu	Arg	Asp	Ile	Gln	Asp	Tyr	Trp	Ile	Ser	Leu	Pro	Gly	Thr	Leu
385				390						395				400	
Cys	Ser	Glu	Lys	Met	Ala	Met	Ser	Pro	Ala	Ser	Asp	Asp	Arg	Cys	Trp
			405						410					415	
Asn	Gly	Ile	Ser	Lys	Gly	Arg	Tyr	Leu	Pro	Glu	Val	Met	Gly	Asp	Gly
			420					425					430		
Leu	Ala	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Glu	Val	Asp	Ile	Thr	Lys
		435					440					445			
Pro	Asp	Met	Thr	Ile	Arg	Gln	Gln	Ile	Met	Gln	Leu	Lys	Ile	Met	Thr
	450					455						460			
Asn	Arg	Leu	Arg	Gly	Ala	Tyr	Gly	Gly	Asn	Asp	Val	Asp	Phe	Gln	Asp
465					470					475				480	
Ala	Ser	Asp	Asp	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Gly	Gly	Cys	Pro	Asp
			485					490						495	
Asp	Ala	Cys	Gly	Arg	Arg	Val	Ser	Lys	Lys	Ser	Ser	Ser	Ser	Arg	Thr
			500					505					510		
Pro	Leu	Thr	His	Ala	Leu	Pro	Gly	Leu	Ser	Glu	Gln	Glu	Gly	Gln	Lys
			515				520					525			

B1
Cont

Thr Ser Ala
530

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTTGCTGT GTGCCTGGTG 60
GCTTTCATGC TATAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTTC TCTTTGCAAT TTTTCTTATC 60
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
1 5 10 15
Ile Phe Leu Ile Leu Leu Val
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTTGCTGC CTCCTTGTC 60
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

B1
Ent

GTCTTGGCAG CTCTGATTGT GGGCGGCGTA GTGGGCATCC TCTTCGCCGT TTTCCTGATC 60
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTTAC CTTGGTCCTT 60
GCTGCAGCCA GGCCCAGGTG GCGGTAAGT CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Thr	Arg	Pro	Glu	Pro	His	Tyr	Phe	Phe	Leu	Leu	Phe	Leu	Phe	Thr
1				5						10				15	
Leu	Val	Leu	Ala	Ala	Ala	Arg	Pro	Arg	Trp	Arg					
			20						25						

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

B1
Cont

Leu Gly Lys Lys Pro Ile Tyr Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT

23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCTCT GGGCGAGTGG GGG

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGAGCTCT TGGAACCATG GCFCCTGTCT GCC

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCAG GTTTTATTAT CTTTTTATC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTATTGGGC GCCGTGTCAC CAGGGC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

B1
cont

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCATGAGC TCCACCACCC TGTTTCG

26

B1
cnt